

SEQUENCE LISTING

Sequencing Report 2003

<110> Mercian Corporation
 <110> Eisai Co., Ltd

<120> DNA related to hydroxylation of macrolide compounds

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<150> JP 2003-396828
 <151> 2003-11-27

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<222> (1322).. (2548)

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caccactgc	gtcgggctgg	gctcgtaactc	gcccctcaagt	ggcaaggat	300
cgtcggctcg	gccccatgggt	ctccggacgg	tcccaactcc	cgccggccgc	360
gtaccgcata	cccccttcggc	cgaggcggtg	atcaccgttc	cgccatccg	420
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cgaggaccag	cgccgaggcc	cagcgcagcg	ggtccagcac	cgcccgccagc	840
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ccgtcacggg	cggtggggac	tggttccccc	ggggacggcg	gcgcgcgcgc	1080
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c atg acg gaa	ctg acg gac	atc acc ggc	ccg ggg acc	ccg gcc gaa	1366
Met Thr Glu	Leu Thr Asp	Ile Thr Gly	Pro Gly Thr	Pro Ala Glu	
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ccc gtc gca ttc	ccc cag gac	cgcc acc tgc	ccc tac cac	ccc ccc acc	1414
Pro Val Ala Phe	Pro Gln Asp	Arg Thr Cys	Pro Tyr His	Pro Pro Thr	
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gga tac ggc	ccg ctg cgc	gac ggg cgc	agc ctg tcc	cgcc gtc acc ctc	1462
Gly Tyr Gly	Pro Leu Arg	Asp Gly Arg	Ser Leu Ser	Arg Val Thr Leu	
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ttc gac ggc	cgc gag gtc	tgg atg gtc	acg ggc cac	gcc acc gcc cgc	1510
Phe Asp Gly	Arg Glu Val	Trp Met Val	Thr Gly His	Ala Thr Ala Arg	

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Ala Leu Ala Asp Pro Arg Leu Ser Thr Asp Arg Thr Leu Pro Gly			1558
65	70	75	
ttc ccc gtc ccc acg gcc cgc ttc gct gcc gtc cgc gac cgg cgg gtc			1606
Phe Pro Val Pro Thr Ala Arg Phe Ala Ala Val Arg Asp Arg Arg Val			
80	85	90	95
gct ctc gct ggc gtc gac gac ccc gtc cac cag acc cag cgg cgg aig			1654
Ala Leu Leu Gly Val Asp Asp Pro Val His Gln Thr Gln Arg Arg Met			
100	105	110	
atg atc ccc tcg ttc acc ctc aag cgc gct ggg ctg cgg ccc acc			1702
Met Ile Pro Ser Phe Thr Leu Lys Arg Ala Ala Gly Leu Arg Pro Thr			
115	120	125	
atc cag cgg acc gtc gac ggg ctg ctg gac gct atg atc gag aag ggg			1750
Ile Gln Arg Thr Val Asp Gly Leu Leu Asp Ala Met Ile Glu Lys Gly			
130	135	140	
ccg ccc gcc gag ctg gtc tcc gcc ttc gcc ctg ccc gtc ccc tcg gtc			1798
Pro Pro Ala Glu Leu Val Ser Ala Phe Ala Leu Pro Val Pro Ser Val			
145	150	155	
gtc atc tgc ggc ctg ctc ggc gtc ccg tac gcc gac cac gag ttc ttc			1846
Val Ile Cys Gly Leu Leu Gly Val Pro Tyr Ala Asp His Glu Phe Phe			
160	165	170	175
gag gaa cag tcc cgc acg ctg ctg cgc ggt ccc acg gcc gcc gac tcg			1894
Glu Glu Gln Ser Arg Thr Leu Leu Arg Gly Pro Thr Ala Ala Asp Ser			
180	185	190	
caa ggg gct cgc gag cgg ctc gag gag tac ctc ggc ggg ctg atc gac			1942
Gln Gly Ala Arg Glu Arg Leu Glu Glu Tyr Leu Gly Gly Leu Ile Asp			
195	200	205	
gac aag gag cgg cag gcc gaa ccc ggc gac ggc gtc ctg gac gac ctc			1990
Asp Lys Glu Arg Gln Ala Glu Pro Gly Asp Gly Val Leu Asp Asp Leu			
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Val His Gln Arg Leu Arg Thr Gly Glu Leu Asp Arg Arg Asp Val Val			
225	230	235	
gct ctg gcc gtc atc ctg ctc gtg gcc ggg cac gag acg acc gcc aac			2086
Ala Leu Ala Val Ile Leu Leu Val Ala Gly His Glu Thr Thr Ala Asn			
240	245	250	255
atg atc tcc ctc ggc acc tac acg ctg ctg cgg cac ccc ggc cgg ctg			2134
Met Ile Ser Leu Gly Thr Tyr Thr Leu Leu Arg His Pro Gly Arg Leu			
260	265	270	
gcc gag ctg cgc gcc gac ccc ggc ctg ctg ccc gcc gtc gag gag			2182
Ala Glu Leu Arg Ala Asp Pro Ala Leu Leu Pro Ala Ala Val Glu Glu			
275	280	285	
ctg atg cgg atg ctc tcg atc gct gac ggg ctg ctg cgc ctg gcc ctg			2230
Leu Met Arg Met Leu Ser Ile Ala Asp Gly Leu Leu Arg Leu Ala Leu			
290	295	300	
gag gac atc gag atc gcc ggc gcc acg atc cgg gcc ggc gag ggc gtc			2278
Glu Asp Ile Glu Ile Ala Gly Ala Thr Ile Arg Ala Gly Glu Gly Val			
305	310	315	
ctg ttc tcc acc tcg ctg atc aac cgc gac gag tcc gtc ttc gac gac			2326
Leu Phe Ser Thr Ser Leu Ile Asn Arg Asp Glu Ser Val Phe Asp Asp			
320	325	330	335
ccc gac acc ctg gac ttc cac cgc tcc acc cgc cac cac gtc gcc ttc			2374
Pro Asp Thr Leu Asp Phe His Arg Ser Thr Arg His His Val Ala Phe			
340	345	350	
ggt ttc ggc atc cac cag tgc ctg ggc gag aac ctg gcc cgc gcc gag			2422
Gly Phe Gly Ile His Gln Cys Leu Gly Gln Asn Leu Ala Arg Ala Glu			
355	360	365	
ctg gag atc gcc ctg ggc acg ctc ctg gag cgg ctc ccc ggc ctc cgg			2470
Leu Glu Ile Ala Leu Gly Thr Leu Leu Glu Arg Leu Pro Gly Leu Arg			
370	375	380	

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Leu Ala Ala Pro Ala Glu Glu lle Pro Phe Lys Pro Gly Asp Thr lle	
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cag ggg atg ctg gaa ctc ccc gtg acc tgg taa gaggctctgg tc atg cac	2569
Gln Gly Met Leu Glu Leu Pro Val Thr Trp	
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lle Asp lle Asp Lys Asp Arg Cys lle Gly Ala Gly Gln Cys Ala Leu	
415 420 425	
gcc gcc ccc ggc gtg ttc acc cag gac gac gac ggc tac agc acc ctg	2665
Ala Ala Pro Gly Val Phe Thr Gln Asp Asp Asp Gly Tyr Ser Thr Leu	
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ctc ccc ggc cgc gag gac ggc ggg ggc gac ccg atg gtc cgg gag gcg	2713
Leu Pro Gly Arg Glu Asp Gly Gly Asp Pro Met Val Arg Glu Ala	
445 450 455	
gcc cgc gcc tgc ccg gtg agc gcc atc ccg gtg acc gaa ccg gcc ggc	2761
Ala Arg Ala Cys Pro Val Ser Ala lle Arg Val Thr Glu Pro Ala Gly	
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gtacaccggcc tacctcggtt acacccagct cggacatgcg ttcggacaga gcctgcccggc	180
cgaggcggca cacgaccgct atctggatgg cgtgatcgac accccatcgatcgccgcggga	240
cgaggcggat gaagccgaaat atgicacaat ctgaacggagg ttggcgaaac tgcgcgcaga	300
acatggccggc tatcccgccgc atgagggttag atcggcgccgg cgaacacgg tgcgcacacag	360

cgttgccatc tcacacacga gcaactcgag ccacttgaga ctctacggg aggaaattc	419
gtg acc gaa gcc atc ccc tac ttt cag aac cgc acc tgt ccc tac cac Val Thr Glu Ala Ile Pro Tyr Phe Gln Asn Arg Thr Cys Pro Tyr His	467
1 5 10 15	
ccg ccc gcc gcc tat cag cca ctg cgc ggg gcc ggc ccc ctg agc cat Pro Pro Ala Ala Tyr Gln Pro Leu Arg Gly Ala Gly Pro Leu Ser His	515
20 25 30	
gtc acg ttc tac gac ggc cgg aag gtg tgg gcg gtc acc ggc cac ccc Val Thr Phe Tyr Asp Gly Arg Lys Val Trp Ala Val Thr Gly His Pro	563
35 40 45	
gag gca cgg gcg ctg ctg acc gac cag cga ctc tcc gcc gac cgg cag Glu Ala Arg Ala Leu Leu Thr Asp Gln Arg Leu Ser Ala Asp Arg Gln	611
50 55 60	
aac ccg gcc ttc ccg gtc ccc ttc gaa cgc ttc gcg gcc atc cgc cgg Asn Pro Ala Phe Pro Val Pro Phe Glu Arg Phe Ala Ala Ile Arg Arg	659
65 70 75 80	
gtc cgg acg ccg ctg atc ggg gtc gac gac ccc gag cac aac acc cag Val Arg Thr Pro Leu Ile Gly Val Asp Asp Pro Glu His Asn Thr Gln	707
85 90 95	
cgc cgg atg ctg atc ccc agc ttc agc ctc aag cgg acc gcc gca ctg Arg Arg Met Leu Ile Pro Ser Phe Ser Leu Lys Arg Thr Ala Ala Leu	755
100 105 110	
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115 120 125	
gat cag ggc ccg ccc acc gag ctg gtc tcc gcc ttc gcc ctg ccc gtc Asp Gln Gly Pro Pro Thr Glu Leu Val Ser Ala Phe Ala Leu Pro Val	851
130 135 140	
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145 150 155 160	
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165 170 175	
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210 215 220	
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225 230 235 240	
aac atg atc tcg ctc ggc acc ttc acc ctg ctg gac cac ccc gag cag Asn Met Ile Ser Leu Gly Thr Phe Thr Leu Leu Asp His Pro Glu Gln	1187
245 250 255	
ctg gcg cag ctc aag gcc gac gag ggc ctg atg ccc ggc gcc atc gag Leu Ala Gln Leu Lys Ala Asp Glu Gly Leu Met Pro Ala Ala Ile Glu	1235
260 265 270	
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275 280 285	
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290 295 300	
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Ala Pro Asp Glu Leu Asp Leu Gly Arg	Ser Ala Arg His His	Val Ala		
325	330	335		
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Ser Gly Phe Gly Ile His Gln Cys Leu	Gly Gln Asn Leu	Ala Arg Ala		
340	345	350		
gag atg gag atc gcg ctg cgc tca	ctg ttc acc agg atc	ccg cag ctg		1523
Glu Met Glu Ile Ala Leu Arg	Ser Leu Phe Thr Arg	Ile Pro Gln Leu		
355	360	365		
cg _g ctc gcc gt _g cc _g g _{cc} g _{ag} att cc _g ttc a _{ag} g _{ac} g _{ga} g _{ac} acc				1571
Arg Leu Ala Val Pro Ala Ala Glu Ile Pro Phe Lys	Asp Gly Asp Thr			
370	375	380		
ctg c _{aa} g _{gc} at _g atc g _{aa} ctg c _{cg} ctg g _{cc} t _{gg} t _{ag} c _{agccaggac} g _{gcaga}				1623
Leu Gln Gly Met Ile Glu Leu Pro Leu Ala Trp				
385	390	395		
ccaaagaaag gggccggaa atg c _{gg} atc g _{cg} atc g _{ac} acc g _{ac} c _{gc} t _{gt} atc				1675
Met Arg Ile Ala Ile Asp Thr Asp Arg Cys Ile				
400	405			
ggc g _{cc} g _{gc} c _{ag} t _{gt} g _{cc} c _{tc} g _{cc} g _{cc} g _{gg} g _{gt} t _{tc} a _{cc} c _{ag} g _{at}				1723
Gly Ala Gly Gln Cys Ala Leu Thr Ala Pro Gly Gly Phe Thr Gln Asp				
410	415	420		
gac g _{ac} g _{gt} t _{tc} a _{gt} g _{ca} c _{tc} c _{cc} g _{gc} c _{gg} g _{ag} g _{ac} g _{gc} g _{cc} g _{gc}				1771
Asp Asp Gly Phe Ser Ala Leu Leu Pro Gly Arg Glu Asp Gly Ala Gly				
425	430	435		
gac c _{cg} c _{tg} g _{tg} c _{gg} g _{aa} g _{cc} g _{cc} c _{gc} g _{cc} t _{gc} c _{cc} g _{tg} c _{ag} g _{cc} a _{tt}				1819
Asp Pro Leu Val Arg Glu Ala Ala Arg Ala Cys Pro Val Gln Ala Ile				
440	445	450		
g _{cg} g _{tc} a _{cc} g _{ac} g _{at} t _{ag} c _{agcacc} c _{ggacgacc} c _{ggcagacgc} g _{cgccggcc}				1875
Ala Val Thr Asp Asp				
455				
ccggctgaca cccggcgccc gaggcgcgcc cgagccgtcc gccccctccac ttgtccctac				1935
ggcatccacc ccatccgc _{ta} c _{cgcaacacc} c _{ttgggtga} c _{gggcagttt} c _{gaggaccc}				1995
gg _{tg} cccg g _{ggcgta} c _{tg} g _{tgcacgtca} c _{ggctticac} g _{ccgcgattt} c _{ccacatagg}				2055
c _{gtcgctcgct} c _{cgccgcgatc} a _{cgaagcgcg} g _{tccggtgccc} c _{ggctcgtaa} c _{ggtgacacga}				2115
t _{gcccggcag} t _{ttccacggtg} a _{accggccgg} c _{acatcg} g _{cccccggcc} g _{ggggccacca}				2175
a _{cagggtgcac} c _{agcgcttc} c _{tgcgcgttgc} g _{ccgcgacatc} g _{tagagcttgc} g _{cgaaacagca}				2235
c _{ccagcttgtc} c _{ccgcgcattc} g _{cgccgcgt} g _{cccccgc} g _{gcctgcggc} g _{aggcaac} c _t				2295
t _{cagcgta} c _{ctcgccgc} c _{ccaccacgt} c _{gac}				2329

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 gggcatctaa t_{gaagatcg} c_{acgcacgt} c_{ttcgcttg} c_{gaggcttcc} c_{atg aca}
 Met Thr
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gac acg aca gac ctg acc gag ctg tca gat ccc gtc tcc ttc ccc cag	225
Asp Thr Thr Asp Leu Thr Glu Leu Ser Asp Pro Val Ser Phe Pro Gln	
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gac cgg agc tgc ccc tac cac ccg ccc acc ggg tac gac ccg ctg cgc	273
Asp Arg Ser Cys Pro Tyr His Pro Pro Thr Gly Tyr Asp Pro Leu Arg	
20 25 30	
acc gaa cgg ccg ccc gcc cgc atc cgg ctc tac gac ggc cgc ccc gcc	321
Thr Glu Arg Pro Pro Ala Arg Ile Arg Leu Tyr Asp Gly Arg Pro Ala	
35 40 45 50	
tgg ctc gtc acc ggc cac gcc gtc cgt gac ctg ctg gtc gac ccc	369
Trp Leu Val Thr Gly His Ala Val Ala Arg Asp Leu Leu Val Asp Pro	
55 60 65	
cgc ctg tcc acg gac cgc acc cgc tcg ggc ttc ccg gcc aca act ccc	417
Arg Leu Ser Thr Asp Arg Thr Arg Ser Gly Phe Pro Ala Thr Thr Pro	
70 75 80	
cgc ttc gcc gcg gtc cgc gac cgc aag ccg gcg ctc ctc ggc gtc gac	465
Arg Phe Ala Ala Val Arg Asp Arg Lys Pro Ala Leu Leu Gly Val Asp	
85 90 95	
gac ccc aag cac cgc acc cag cgg tgg atg atg atc ccg agc ttc acc	513
Asp Pro Lys His Arg Thr Gln Arg Trp Met Met Ile Pro Ser Phe Thr	
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ctc agg cgc gcc acc gag ctc agg ccg cgc atc cag gag atc gtc gac	561
Leu Arg Arg Ala Thr Glu Leu Arg Pro Arg Ile Gln Glu Ile Val Asp	
115 120 125 130	
gaa ctg ctg gac gtc atg atc gcc cag gga ccc ccg gcc gac ctg gtc	609
Glu Leu Leu Asp Val Met Ile Ala Gln Gly Pro Pro Ala Asp Leu Val	
135 140 145	
cgt tcc ttc gcg ctg ccg gtc tcc atg gtc atc tgc gcc ctg ctc	657
Arg Ser Phe Ala Leu Pro Val Pro Ser Met Val Ile Cys Ala Leu Leu	
150 155 160	
ggc gtg ccc tac gcc gac cac gag ttc ttc gag gac cag tcc agg cgg	705
Gly Val Pro Tyr Ala Asp His Glu Phe Phe Glu Asp Gln Ser Arg Arg	
165 170 175	
ctg ctg cgc gga ccg gcg gcc gag gac acg cag gac gcc cgg gac cgg	753
Leu Leu Arg Gly Pro Ala Ala Glu Asp Thr Gln Asp Ala Arg Asp Arg	
180 185 190	
ctc gcc gcg tac ctg gag gac ctg atc gac gag aag cgg cgc cgg ccc	801
Leu Ala Ala Tyr Leu Glu Asp Leu Ile Asp Glu Lys Arg Arg Arg Pro	
195 200 205 210	
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Gly Asp Gly Leu Leu Asp Glu Leu Val Gln Gln Arg Leu Asn Glu Gly	
215 220 225	
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Glu Leu Asp Arg Glu Glu Leu Thr Ala Leu Ala Met Ile Leu Leu Val	
230 235 240	
gcg ggc cac gag acc acc gcc aac atg atc tcc ctg ggc acc tac acg	945
Ala Gly His Glu Thr Thr Ala Asn Met Ile Ser Leu Gly Thr Tyr Thr	
245 250 255	
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Leu Leu Leu His Pro Glu Arg Leu Thr Glu Leu Arg Ala Asp Pro Ala	
260 265 270	
ctg ctg ccc gcc gtc gag gaa ctg atg cgg atg ctg tcc atc gcg	1041
Leu Leu Pro Ala Ala Val Glu Glu Leu Met Arg Met Leu Ser Ile Ala	
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Asp Gly Leu Leu Arg Gln Ala Thr Glu Asp Ile Glu Ile Ala Gly Thr	
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acc atc agg gcc ggg gac ggc gtg gtc ttc tcc acc tct gtc atc aac	1137
Thr Ile Arg Ala Gly Asp Gly Val Val Phe Ser Thr Ser Val Ile Asn	
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cgc gac gag gac gtc tac ccg gcc ccc gac acc ctc gac ttc cac cgc	1185

Arg Asp Glu Asp Val Tyr Pro Ala Pro Asp Thr Leu Asp Phe His Arg			
325	330	335	
tcg acc cgc cac cac gtc gcc ttc ggt ttc gga atc cac cag tgc ctc			1233
Ser Thr Arg His His Val Ala Phe Gly Phe Gly Ile His Gln Cys Leu			
340	345	350	
ggc cag aac ctc gcc cgc acc gaa ctg gag atc gcc ctg cgc acg ctc			1281
Gly Gln Asn Leu Ala Arg Thr Glu Leu Glu Ile Ala Leu Arg Thr Leu			
355	360	365	370
ctc gaa cgg ctg ccc acg ctc cgg ctc gcc gcc cca ccg gag gaa atc			1329
Leu Glu Arg Leu Pro Thr Leu Arg Leu Ala Ala Pro Pro Glu Glu Ile			
375	380	385	
ccc ttc aaa ccc ggc gac acc atc cag ggg atg ctg gaa ctc ccc gtc			1377
Pro Phe Lys Pro Gly Asp Thr Ile Gln Gly Met Leu Glu Leu Pro Val			
390	395	400	
agc tgg taa gaggctgccc tc atg cat atc gag atc gac aag gac cgc tgc			1428
Ser Trp Met His Ile Glu Ile Asp Lys Asp Arg Cys			
405	410		
atc ggc gcc gga cag tgc gcc ctg acc gcc ccg ggt gtg ttc acc cag			1476
Ile Gly Ala Gly Gln Cys Ala Leu Thr Ala Pro Gly Val Phe Thr Gln			
420	425	430	
gac gac gac ggc ttc agt gac ctg ttg ccc ggc ccg gag gac ggc gcc			1524
Asp Asp Asp Gly Phe Ser Asp Leu Leu Pro Gly Arg Glu Asp Gly Ala			
415	435	440	445
ggc gac ccg atg gtc cgg gag gcc gcc agg gcc tgc ccc gtg agt gcc			1572
Gly Asp Pro Met Val Arg Glu Ala Ala Arg Ala Cys Pro Val Ser Ala			
450	455	460	
atc acg ctg tcc gag gac ggg tag gggggccgagc cgcgcgcgc cccgggtccgc			1626
Ile Thr Leu Ser Glu Asp Gly			
465			
tgccgcggcg ccgtgccgac gcggcggccg gccggccgt ccgggtgcgg tcgcgtcgcc			1686
ccgtggccccc ggcggcgct gattgactag gttcccggt tgagcgaaca ggcccagaag			1746
ccctccgggg cggccggccgc gaaagacacc gggacggcgc cgggaaacc ctttcctcta			1806
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